

RESULT 1

AAW98314

ID AAW98314 standard; protein; 285 AA.

XX

AC AAW98314;

XX

DT 15-JUN-2007 (revised)

DT 31-MAR-1999 (first entry)

XX

DE H. pylori GHPO 894 protein.

XX

KW GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;

KW peptic ulcer disease; BOND_PC;

KW siderophore-mediated iron transport protein (tonB); GO5381; GO6810;

KW GO6826; GO8565; GO15031; GO16020; GO16021; GO30288; GO42597.

XX

OS Helicobacter pylori.

XX

PN WO9843478-A1.

XX

PD 08-OCT-1998.

XX

PF 01-APR-1998; 98WO-US006371.

XX

PR 01-APR-1997; 97US-00833457.

PR 24-JUN-1997; 97US-00881227.

PR 29-JUL-1997; 97US-00902615.

XX

PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Kleanthous H, Al-Garawi A, Miller C, Tomb J, Oomen RP;

XX

DR WPI; 1998-542293/46.

DR N-PSDB; AAX14033.

DR PC:NCBI; gi3915142.

DR PC:SWISSPROT; O25899.

XX

PT New isolated Helicobacter polynucleotides - used to develop products for

PT the diagnosis, prevention and treatment of Helicobacter infections and

PT gastrointestinal diseases.

XX

PS Claim 8; Page 413-415; 2054pp; English.

XX

CC This sequence represents a Helicobacter pylori GHPO protein of the

CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroduodenal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for
CC detection and diagnosis
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 285 AA;

Query Match 100.0%; Score 1453; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.1e-100;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1
MKISPSRKLSKVSTSVSFLISFALYAIGFGYFLLREDAPEPLAQAGTTKVTMSLAS
INT 60

|||||

Db 1
MKISPSRKLSKVSTSVSFLISFALYAIGFGYFLLREDAPEPLAQAGTTKVTMSLAS
INT 60

Qy 61
NSNTKTNAESAKPKEEPKEKPKKEEPKKEEPKKEVTKPKPKPKPKPKPKPKPE
PKPEP 120

|||||

Db 61
NSNTKTNAESAKPKEEPKEKPKKEEPKKEEPKKEVTKPKPKPKPKPKPKPKPE
PKPEP 120

Qy 121
KPEPKPEPKVEEVKKEEPKEEPKKEEAKKEEAKESAPKQVTTKDIVKEKDKQEE
NKTSE 180

|||||

Db 121
KPEPKPEPKVEEVKKEEPKEEPKKEEAKKEEAKESAPKQVTTKDIVKEKDKQEE
NKTSE 180

Qy 181
GATSEAQAYNPGVSNEFLMKIQTAISSKNRYPKMAQIRGIEGEVLVSFTINADGS
VTDIK 240

|||||

Db 181
GATSEAQAYNPGVSNEFLMKIQTAISSKNRYPKMAQIRGIEGEVLVSFTINADGS
VTDIK 240

Qy 241 VVKSNTTDILNHAALAIKSAAHLFPKPEETVHLKIPIAYSLKED 285
|||||

Db 241 VVKSNTTDILNHAALAIKSAAHLFPKPEETVHLKIPIAYSLKED 285